

# WEST Search History





DATE: Wednesday, July 11, 2007

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		<i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>	
<input type="checkbox"/>	L9	p116 with (IRES or HCV or hepatitis adj C) AND (eIF3 or eukaryotic adj initiation adj factor near3 3)	1
<input type="checkbox"/>	L8	L6 and p116 same (IRES or HCV or hepatitis adj C)	2
<input type="checkbox"/>	L7	L6 and p116	6
<input type="checkbox"/>	L6	(eIF3 or eukaryotic adj initiation adj factor near3 3) same (HCV or hepatitis adj c)	17
<input type="checkbox"/>	L5	(bicistronic or bi-cistronic) same luciferase same translat\$ and (@ad<20021212 or @pd<20021212)	36
<input type="checkbox"/>	L4	L3 and (@ad<20021212 or @pd<20021212)	46
<input type="checkbox"/>	L3	L2 and translat\$	96
<input type="checkbox"/>	L2	(bicistronic or bi-cistronic) same luciferase	104
<input type="checkbox"/>	L1	20060035212 .pn. and rrm	1

END OF SEARCH HISTORY


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## Search

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Time Result

<a href="#">#14</a> Search <b>#9 AND #13</b>	11:30:33	<a href="#">65</a>
<a href="#">#13</a> <b>Related Articles for PubMed (Select 11410661)</b>	11:25:03	<a href="#">469</a>
<a href="#">#8</a> Search <b>#2 AND (II or IIab)</b>	11:24:24	<a href="#">4</a>
<a href="#">#3</a> Search <b>#2 AND p116</b>	11:24:18	<a href="#">4</a>
<a href="#">#9</a> <b>Related Articles for PubMed (Select 9628916)</b>	11:24:08	<a href="#">118</a>
<a href="#">#11</a> Search <b>balakireva[au] AND (eIF3 or HCV or "hepatitis c" or "eukaryotic translation initiation factor" or "eukaryotic initiation factor ")</b>	11:21:46	<a href="#">0</a>
<a href="#">#10</a> Search <b>balakireva[au] AND (eIF3 or HCV or "hepatitis c" or "eukaryotic translation initiation factor" or "eukaryotic initiation factor ")</b>	11:21:17	<a href="#">350</a>
<a href="#">#2</a> Search <b>(eIF3 or "eukaryotic initiation factor 3") AND (HCV or "hepatitis C")</b>	11:12:55	<a href="#">28</a>
<a href="#">#1</a> <b>Related Articles for PubMed (Select 9780040)</b>	10:57:22	<a href="#">131</a>

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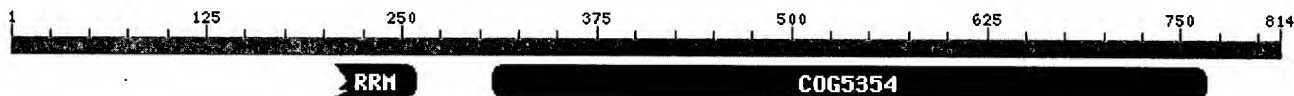
# BLAST Basic Local Alignment Search Tool

Job Title: AAI10866:Eukaryotic translation initiation...

3c

## Show Conserved Domains

Putative conserved domains have been detected, click on the image below for detailed results.



BLASTP 2.2.17 (Jun-24-2007)

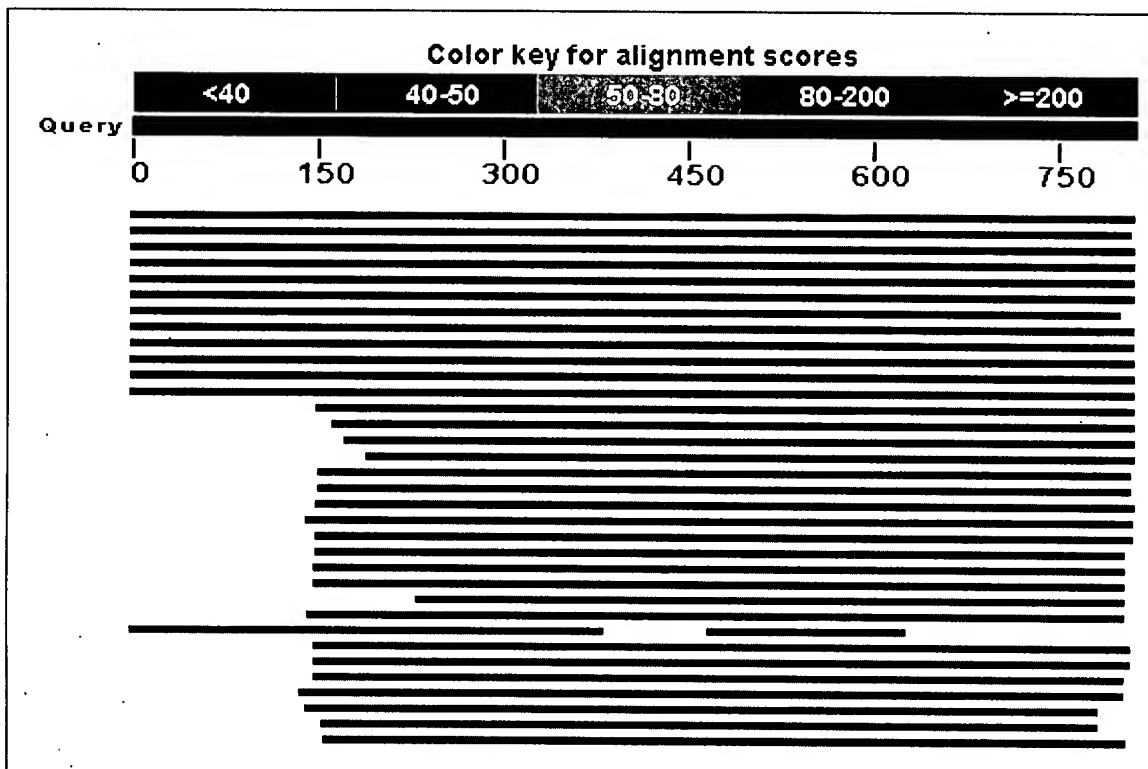
**Reference:** Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

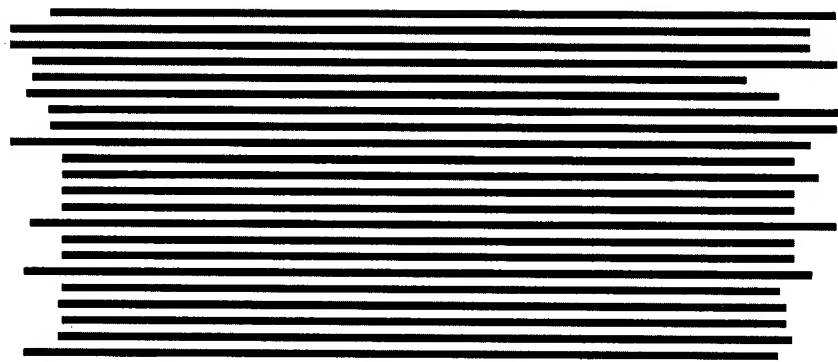
**Reference:** Schäffer, Alejandro A., L. Aravind, Thomas L. Madden, Sergei Shavirin, John L. Spouge, Yuri I. Wolf, Eugene V. Koonin, and Stephen F. Altschul (2001), "Improving the accuracy of PSI-BLAST protein database searches with composition-based statistics and other refinements", Nucleic Acids Res. 29:2994-3005. RID: 9AB7KR8V014 **Database:** All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects 5,269,953 sequences; 1,825,351,362 total letters

**Query=** gi|3123230|sp|P55884|IF39\_HUMAN Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p116) (eIF3 p110) (eIF3b) (Prt1 homolog) (hPrt1) Length=814

*L equivalent to SEA 10 no:4*

## Distribution of 101 Blast Hits on the Query Sequence





Distance tree of results <sup>NEW</sup> Related Structures

Sequences producing significant alignments:		Score (Bits)	E Value	
<a href="#">ref XP_001086876.1 </a>	PREDICTED: eukaryotic translation initiat...	1582	0.0	<b>UG</b>
<a href="#">gb AAB42010.1 </a>	Prt1 homolog [Homo sapiens]	1580	0.0	<b>UG</b>
<a href="#">sp P55884 IF39_HUMAN</a>	Eukaryotic translation initiation factor...	1578	0.0	<b>G</b>
<a href="#">ref NP_003742.2 </a>	eukaryotic translation initiation factor 3, ...	1576	0.0	<b>UG</b>
<a href="#">gb EAW87239.1 </a>	eukaryotic translation initiation factor 3, su...	1570	0.0	<b>G</b>
<a href="#">gb EAL23952.1 </a>	eukaryotic translation initiation factor 3, su...	1528	0.0	<b>G</b>
<a href="#">gb AAH23767.1 </a>	Eif3s9 protein [Mus musculus] > <a href="#">gb AAH51065.1 </a> ...	1451	0.0	<b>UG</b>
<a href="#">ref NP_598677.1 </a>	eukaryotic translation initiation factor 3, ...	1437	0.0	<b>UG</b>
<a href="#">ref NP_001026810.1 </a>	eukaryotic translation initiation factor ...	1425	0.0	<b>UG</b>
<a href="#">ref XP_001256599.1 </a>	PREDICTED: similar to eukaryotic translat...	1398	0.0	<b>UG</b>
<a href="#">ref XP_001379111.1 </a>	PREDICTED: similar to eukaryotic translat...	1354	0.0	<b>G</b>
<a href="#">ref XP_850719.1 </a>	PREDICTED: similar to Eukaryotic translation...	1349	0.0	<b>UG</b>
<a href="#">ref XP_536894.2 </a>	PREDICTED: similar to Eukaryotic translation...	1335	0.0	<b>UG</b>
<a href="#">ref XP_001513573.1 </a>	PREDICTED: similar to eukaryotic translat...	1316	0.0	<b>G</b>
<a href="#">gb AAH07175.1 </a>	Eif3s9 protein [Mus musculus]	1307	0.0	<b>UG</b>
<a href="#">gb AAH09986.1 AAH09986</a>	Unknown (protein for IMAGE:4124553) [Homo	1276	0.0	<b>UG</b>
<a href="#">ref NP_001090004.1 </a>	hypothetical protein LOC735075 [Xenopus l...	1246	0.0	<b>UG</b>
<a href="#">ref NP_001016724.1 </a>	eukaryotic translation initiation factor ...	1223	0.0	<b>UG</b>
<a href="#">ref XP_862133.1 </a>	PREDICTED: similar to Eukaryotic translation...	1221	0.0	<b>UG</b>
<a href="#">ref XP_001335480.1 </a>	PREDICTED: similar to Prt1 homolog [Danio re	1206	0.0	<b>UG</b>
<a href="#">emb CAF92736.1 </a>	unnamed protein product [Tetraodon nigroviridis]	1090	0.0	
<a href="#">ref XP_001190551.1 </a>	PREDICTED: similar to Prt1 homolog [Stron...	899	0.0	<b>UG</b>
<a href="#">ref XP_393588.2 </a>	PREDICTED: similar to eIF3-S9 CG4878-PB, iso...	820	0.0	<b>UG</b>
<a href="#">ref XP_972849.1 </a>	PREDICTED: similar to CG4878-PB, isoform B [...	800	0.0	<b>UG</b>
<a href="#">ref XP_796053.2 </a>	PREDICTED: similar to Prt1 homolog, partial ...	791	0.0	<b>UG</b>
<a href="#">ref NP_001037602.1 </a>	eIF3-S9 [Bombyx mori] > <a href="#">gb ABF55967.1 </a> eIF3-S	732	0.0	<b>UG</b>
<a href="#">gb AAP21880.1 </a>	unknown [Homo sapiens]	695	0.0	<b>G</b>
<a href="#">gb AAM52578.1 </a>	AT09438p [Drosophila melanogaster]	685	0.0	<b>U</b>
<a href="#">ref NP_611228.1 </a>	eIF3-S9 CG4878-PB, isoform B [Drosophila mel...	685	0.0	<b>UG</b>
<a href="#">gb EAT40558.1 </a>	translation initiation factor 3, subunit S9, p...	682	0.0	
<a href="#">ref XP_320387.2 </a>	ENSANGP00000013937 [Anopheles gambiae str. P...	656	0.0	<b>G</b>
<a href="#">emb CAN76773.1 </a>	hypothetical protein [Vitis vinifera]	528	7e-148	
<a href="#">gb ABE81765.1 </a>	Translation initiation factor eIF-3b [Medicago tr	516	3e-144	
<a href="#">ref NP_568498.1 </a>	TIF3B1 (EUKARYOTIC TRANSLATION INITIATION FA...	513	2e-143	<b>G</b>
<a href="#">ref NP_568477.1 </a>	EIF3B-2 (eukaryotic translation initiation f...	511	9e-143	<b>G</b>
<a href="#">gb EAY79580.1 </a>	hypothetical protein OsI_033539 [Oryza sativa ...	510	2e-142	
<a href="#">ref NP_001065446.1 </a>	Os10g0569200 [Oryza sativa (japonica cult...	502	5e-140	<b>UG</b>
<a href="#">ref NP_001031954.1 </a>	TIF3B1 (EUKARYOTIC TRANSLATION INITIATION...	501	9e-140	<b>G</b>
<a href="#">emb CAL57606.1 </a>	Translation initiation factor 3, subunit b (e...	496	2e-138	
<a href="#">ref XP_001421305.1 </a>	predicted protein [Ostreococcus lucimarin...	496	3e-138	<b>G</b>
<a href="#">sp P56821 IF39_TOBAC</a>	Eukaryotic translation initiation factor...	496	3e-138	
<a href="#">gb AAF67758.1 AF255680.1</a>	eIF3b [Arabidopsis thaliana]	484	7e-135	<b>U</b>
<a href="#">gb EA217037.1 </a>	hypothetical protein OsJ_031246 [Oryza sativa ...	480	2e-133	
<a href="#">ref XP_001389047.1 </a>	hypothetical protein An01g06230 [Aspergil...	478	1e-132	<b>G</b>
<a href="#">ref XP_001214066.1 </a>	hypothetical protein ATEG_04888 [Aspergil...	473	2e-131	<b>G</b>
<a href="#">ref XP_001269939.1 </a>	eukaryotic translation initiation factor ...	473	3e-131	<b>G</b>

dbj BAE55898.1	unnamed protein product [Aspergillus oryzae]	471	9e-131	
ref XP_760446.1	hypothetical protein UM04299.1 [Ustilago may...	470	1e-130	G
ref XP_749953.1	eukaryotic translation initiation factor 3 s...	469	4e-130	G
ref XP_001265448.1	eukaryotic translation initiation factor ...	468	6e-130	G
gb EDN06756.1	hypothetical protein HCAG_03286 [Ajellomyces caps	468	9e-130	
ref XP_657963.1	hypothetical protein AN0359.2 [Aspergillus n...	467	2e-129	G
gb EDN32761.1	hypothetical protein BC1G_11866 [Botryotinia fuck	464	1e-128	
gb EAU93076.1	hypothetical protein CC1G_06796 [Coprinopsis c...	441	7e-122	
ref XP_001226218.1	conserved hypothetical protein [Chaetomiu...	441	1e-121	G
ref XP_001238944.1	hypothetical protein CIMG_09966 [Coccidio...	439	3e-121	G
ref XP_001385934.1	predicted protein [Pichia stipitis CBS 60...	437	1e-120	G
ref XP_505484.1	hypothetical protein [Yarrowia lipolytica] >...	436	3e-120	G
ref XP_365276.1	hypothetical protein MGG_01978 [Magnaporthe ...	436	3e-120	UG
ref XP_959527.1	hypothetical protein [Neurospora crassa OR74...	435	6e-120	G
ref XP_001523611.1	hypothetical protein LELG_05027 [Lodderom...	435	7e-120	G
ref NP_594528.1	hypothetical protein SPAC25G10.08 [Schizosac...	428	8e-118	G
ref XP_639023.1	hypothetical protein DDBDRAFT_0218512 [Dicty...	426	3e-117	G
ref XP_385953.1	conserved hypothetical protein [Gibberella zeae	426	4e-117	G
ref XP_001481981.1	hypothetical protein PGUG_05744 [Pichia g...	418	7e-115	G
ref XP_460786.1	hypothetical protein DEHA0F10681g [Debaryomy...	409	4e-112	
gb AAN75171.2	PRT1 [Cryptococcus neoformans var. grubii]	408	7e-112	
ref XP_570498.1	hypothetical protein [Cryptococcus neoforman...	408	9e-112	UG
gb AAV28786.1	PRT1p [Cryptococcus gattii]	407	1e-111	
gb AAN75151.2	PRT1 [Cryptococcus neoformans var. grubii]	404	1e-110	
gb AAV28752.1	PRT1p [Cryptococcus gattii]	401	1e-109	
ref XP_721420.1	hypothetical protein Ca019.6584 [Candida alb...	400	1e-109	G
gb AAN75610.2	PRT1 [Cryptococcus neoformans var. neoformans]	397	2e-108	
ref NP_001022469.1	Eukaryotic Initiation Factor family membe...	375	5e-102	UG
emb CAE60607.1	Hypothetical protein CBG04247 [Caenorhabditis br	366	3e-99	
ref NP_984494.1	ADR399Cp [Ashbya gossypii ATCC 10895] >gb AA...	358	9e-97	G
ref XP_451155.1	unnamed protein product [Kluyveromyces lacti...	355	9e-96	G
dbj BAD92618.1	eukaryotic translation initiation factor 3, s...	345	8e-93	UG
ref NP_015006.1	Prt1p [Saccharomyces cerevisiae] >sp P06103 ...	340	3e-91	G
gb AAX27752.2	SJCHGC06669 protein [Schistosoma japonicum]	321	1e-85	UG
ref XP_448652.1	unnamed protein product [Candida glabrata] >...	308	9e-82	G
ref XP_763903.1	hypothetical protein TP04_0268 [Theileria pa...	304	1e-80	G
ref XP_729404.1	hypothetical protein PY01620 [Plasmodium yoe...	303	2e-80	G
ref XP_952937.1	eukaryotic translation initiation factor [Th...	303	3e-80	G
ref XP_679842.1	eukaryotic translation initiation factor 3 s...	301	2e-79	G
gb EDL44054.1	Eukaryotic translation initiation factor 3 sub...	301	2e-79	
ref XP_741862.1	eukaryotic translation initiation factor 3 s...	294	1e-77	G
ref XP_667222.1	hypothetical protein Chro.20043 [Cryptospori...	293	4e-77	G
ref XP_001351734.1	eukaryotic translation initiation factor ...	292	5e-77	G
ref XP_625404.1	prtip-like IF39 eukaryotic translation initi...	291	1e-76	G
gb AAS92516.1	PRT1; NFS1 [Cryptococcus gattii]	267	2e-69	
dbj BAC86636.1	unnamed protein product [Homo sapiens]	249	7e-64	G
pdb 2NLW A	unnamed protein product [Homo sapiens]	218	1e-54	S
gb EAT88564.1	hypothetical protein SNOG_03359 [Phaeosphaeria no	196	5e-48	
gb ABD98042.1	translation initiation factor [Striga asiatica]	185	9e-45	
ref XP_001033223.2	hypothetical protein TTHERM_00443100 [Tet...	154	3e-35	G
gb EDM03125.1	rCG62266 [Rattus norvegicus]	152	8e-35	
ref NP_564538.1	eukaryotic translation initiation factor-rel...	145	1e-32	UG

gb|AAF69714.1|AC016041\_19 F27J15.19 [Arabidopsis thaliana] 135 2e-29

ref|XP\_651295.1| hypothetical protein 172.t00009 [Entamoeba h... 133 4e-29 **G**

Alignments

>ref|XP\_001086876.1| **UG** PREDICTED: eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa [Macaca mulatta]  
Length=814

Score = 1582 bits (4095), Expect = 0.0, Method: Composition-based stats.  
Identities = 803/814 (98%), Positives = 806/814 (99%), Gaps = 0/814 (0%)

Query	1	MQDAENVAVPEAAEERAEPGQQQPAAEPPPAEGLLRPAGPGAPEAAAGTEASSEEVGIAEA	60
Sbjct	1	.....D.....AV...	60
Query	61	GPEPEVRTEPAAEAEEAASGPSESPPPAEEELPGSHAEPVPAQGEAPGEQARDERSDSR	120
Sbjct	61	.....F.....L.....P.....R.....CA...	120
Query	121	AQAVSEDAGGNEGRAAAEAPRALENGDADEPSFSDPEDFVDDVSEEELLGDVLKDRPQEA	180
Sbjct	121	...A.....S.....	180
Query	181	DGIDSVIVVDNVPQVGPDRLEKLKNVIHKIFSKFGKITNDFYPEEDGKTKGYIFLEYASP	240
Sbjct	181	.....	240
Query	241	AHAVDAVKNADGYKLDKQHTFRVNLFTDFDKYMTISDEWDIPEKQPFKDLGNLRYWLEEA	300
Sbjct	241	.....	300
Query	301	ECRDQYSVIFESGDRTSIFWNDVKDPVSIEERARWTETYVRWSPKGTYLATFHQRGIALW	360
Sbjct	301	.....	360
Query	361	GGEKFKQIQRFHQVQLIDFSPCERYLVTFSPPLMDTQDDPQAIIIWDILTGHKKRGFHC	420
Sbjct	361	.....	420
Query	421	ESSAHWPIFKWSDGKFFARMTLDTLISIYETPSMGLLDKKSLSKISGIKDFSWSPGGNIIA	480
Sbjct	421	.....	480
Query	481	FWVPEDKDIPARVTLMLPTRQEIRVRNLFNVVDCKLHWQKNGDYLCVKVDRTPKGTQGV	540
Sbjct	481	.....	540
Query	541	VTNFEIFRMREKQVPVDVEMKETIIAFAWEPNGSKFAVLHGEAPRISVSFYHVKNNGKI	600
Sbjct	541	.....	600
Query	601	ELIKMFDKQQANTIFWSPQGQFVVLAGLRSMNGALAFVDTSDCTVMNIAEHYMASDVEWD	660
Sbjct	601	.....	660
Query	661	PTGRYVVTSVSWWSHKVDNAYWLWTFQGRLLQKNNKDRFCQLLWRPRPPTLLSQEQIKQI	720
Sbjct	661	.....	720
Query	721	KKDLKKYSKIFEQKDRLSQSKASKELVERRRTMMEDFRKYRKMAQELYMEQKNERLELRG	780
Sbjct	721	.....	780
Query	781	GVDTDELDSNVDDWEEETIEFFVTEEIIPLGNQE	814
Sbjct	781	.....	814

>gb|AAB42010.1| **UG** Prt1 homolog [Homo sapiens]  
Length=873

Score = 1580 bits (4090), Expect = 0.0, Method: Composition-based stats.  
Identities = 809/811 (99%), Positives = 809/811 (99%), Gaps = 0/811 (0%)

Query	1	MQDAENVAVPEAAEERAEPGQQQPAAEPPPAEGLLRPAGPGAPEAAAGTEASSEEVGIAEA	60
Sbjct	1	.....	60
Query	61	GPEPEVRTEPAAEAEEAASGPSESPPPAEEELPGSHAEPVPAQGEAPGEQARDERSDSR	120
Sbjct	61	.....AG.....	120
Query	121	AQAVSEDAGGNEGRAAAEAPRALENGDADEPSFSDPEDFVDDVSEEELLGDVLKDRPQEA	180
Sbjct	121	.....	180
Query	181	DGIDSVIVVDNVPQVGPDRLEKLKNVIHKIFSKFGKITNDFYPEEDGKTKGYIFLEYASP	240
Sbjct	181	.....	240
Query	241	AHAVDAVKNADGYKLDKQHTFRVNLFTDFDKYMTISDEWDIPEKQPFKDLGNLRYWLEEA	300

Sbjct	241	.....	300
Query	301	ECRDQYSVIFESGDRSIFWNDVKDPVSIEERARWTETYVRWSPKGYLATFHQRGIALW	360
Sbjct	301	.....	360
Query	361	GGEKFKQIQRFHQGVQLIDFSPCERYLVTFSPMLDTQDDPQAIIIWDILTGHKKRGFHC	420
Sbjct	361	.....	420
Query	421	ESSAHWPIFKWSDGKFFARMTLDLSIYETPSMGLLDKKSLKISGIKDFSWSPPGNIIA	480
Sbjct	421	.....	480
Query	481	FWVPEDKDIPARVTLMQLPTRQEIRVRNLFNVVDCKLHWQKNGDYLCVKVDRTPKGTQGV	540
Sbjct	481	.....	540
Query	541	VTNFEIFRMREKQVPVDVEMKETIIAFAWEPNGSKFAVLHGEAPRISVSFYHVKNNGKI	600
Sbjct	541	.....	600
Query	601	ELIKMFDKQQANTIFWSPQGQFVVLAGLRSMNGALAFVDTSDCTVMNIAEHYMASDVEWD	660
Sbjct	601	.....	660
Query	661	PTGRYVVTSSVSWSHKVDNAYWLWTFQGRLLQKNNKDRFCQLLWRPRPPTLLSQEQIKQI	720
Sbjct	661	.....	720
Query	721	KKDLKKYSKIFEQKDRLSQSKASKELVERRRTMMEDFRKYRKMAQELYMEQKNERLELRG	780
Sbjct	721	.....	780
Query	781	GVDTDELDSNVDDWEEETIEFFVTEEIPLG	811
Sbjct	781	.....	811

>sp|P55884|IF39\_HUMAN **G** Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p116) (eIF3 p110) (eIF3b) (Prt1 homolog) (hPrt1)  
 gb|AAC99479.1| **UG** eukaryotic translation initiation factor [Homo sapiens]  
 gb|AAH01173.1| **UG** EIF3S9 protein [Homo sapiens]  
 gb|AAI10866.1| **UG** Eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa [Homo sapiens]  
 Length=814

Score = 1578 bits (4086), Expect = 0.0, Method: Composition-based stats.  
 Identities = 814/814 (100%), Positives = 814/814 (100%), Gaps = 0/814 (0%)

Query	1	MQDAENVAVPEAAEERAEPGQQQPAEPPPAEGLLRPAGPGAPEAAAGTEASSEEVGIAEA	60
Sbjct	1	.....	60
Query	61	GPEPEVRTEPAEAEAAAGPSESPPPAEELPGSHAEPVPAQGEAPGEQARDERSDSR	120
Sbjct	61	.....	120
Query	121	AQAVSEDAGGNEGRAEAEPRALENGDADEPSFSDPEDFVDDVSEELLGDVLKDRPQEA	180
Sbjct	121	.....	180
Query	181	DGIDSVIVVDNVPQVGPDRLEKLKNVIHKIFSKFGKITNDFYPEEDGKTKGYIFLEYASP	240
Sbjct	181	.....	240
Query	241	AHAVDAVKNADGYKLDKQHTFRVNLFTDFDKYMTISDEWDIPEKQPFKDLGNLRYWLEEA	300
Sbjct	241	.....	300
Query	301	ECRDQYSVIFESGDRSIFWNDVKDPVSIEERARWTETYVRWSPKGYLATFHQRGIALW	360
Sbjct	301	.....	360
Query	361	GGEKFKQIQRFHQGVQLIDFSPCERYLVTFSPMLDTQDDPQAIIIWDILTGHKKRGFHC	420
Sbjct	361	.....	420
Query	421	ESSAHWPIFKWSDGKFFARMTLDLSIYETPSMGLLDKKSLKISGIKDFSWSPPGNIIA	480
Sbjct	421	.....	480
Query	481	FWVPEDKDIPARVTLMQLPTRQEIRVRNLFNVVDCKLHWQKNGDYLCVKVDRTPKGTQGV	540
Sbjct	481	.....	540
Query	541	VTNFEIFRMREKQVPVDVEMKETIIAFAWEPNGSKFAVLHGEAPRISVSFYHVKNNGKI	600
Sbjct	541	.....	600
Query	601	ELIKMFDKQQANTIFWSPQGQFVVLAGLRSMNGALAFVDTSDCTVMNIAEHYMASDVEWD	660
Sbjct	601	.....	660
Query	661	PTGRYVVTSSVSWSHKVDNAYWLWTFQGRLLQKNNKDRFCQLLWRPRPPTLLSQEQIKQI	720
Sbjct	661	.....	720
Query	721	KKDLKKYSKIFEQKDRLSQSKASKELVERRRTMMEDFRKYRKMAQELYMEQKNERLELRG	780



Sbjct 721 ..... 780

Query 781 GVDTDELDSNVDDWEEETIEFFVTEEIPLGNQE 814

Sbjct 781 ..... 814

>ref|NP\_003742.2| **UG** eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa  
[Homo sapiens]

ref|NP\_001032360.1| **UG** eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa  
[Homo sapiens]

gb|EAL23951.1| **G** eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa  
[Homo sapiens]

gb|EAW87237.1| **G** eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa,  
isoform CRA\_a [Homo sapiens]

gb|EAW87240.1| **G** eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa,  
isoform CRA\_a [Homo sapiens]

gb|EAW87241.1| **G** eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa,  
isoform CRA\_a [Homo sapiens]  
Length=814

Score = 1576 bits (4080), Expect = 0.0, Method: Composition-based stats.  
Identities = 813/814 (99%), Positives = 813/814 (99%), Gaps = 0/814 (0%)

Query	1	MQDAENVAVPEAAEERAEPGQQQPAAEPPPAEGLLRPAGPGAPEAAAGTEASSEEVGIAEA	60
Sbjct	1	.....	60
Query	61	GPEPEVRTEPAEAEAAASGPSESPPAAEELPGSHAEPVPAQGEAPGEQARDERSDSR	120
Sbjct	61	...S.....	120
Query	121	AQAVSEDAGGNEGRAAEAEPRALENGDADEPSFSDPEDFVDDVSEEEELGDLVKDRPQEA	180
Sbjct	121	.....	180
Query	181	DGIDSVIVVDNVPQVGPDRLKLNVIHKIFSKFGKITNDFYPEEDGKTGKIIFLEYASP	240
Sbjct	181	.....	240
Query	241	AHAVDAVKNADGYKLDKQHTFRVNLFTDFDKYMTISDEWDIPEKQPFKDLGNLRYWLEEA	300
Sbjct	241	.....	300
Query	301	ECRDQYSVIFESGDRTSIFWNDVKDPVSIEERARWTETYVRWSPKGTYLATFHQRGIALW	360
Sbjct	301	.....	360
Query	361	GGEKFKQIQRFSSHQGVQLIDFSPCERYLVTFSPMLDTQDDPQAIIIWDILTGHKKRGFHC	420
Sbjct	361	.....	420
Query	421	ESSAHWPIFKWSDGKFFARMTLDTLSTIYETPSMGLLDKSKSLKISGIKDFSWSPPGNIIA	480
Sbjct	421	.....	480
Query	481	FWVPEDKDI PARVTLMQLPTRQEIRVRNLFNVVDCKLHWQKNGDYLCVKVDRTPKGTQGV	540
Sbjct	481	.....	540
Query	541	VTNFEIFRMREKQVPVDVEMKETIIAFAWEPNGSKFAVLHGEAPRISVSFYHVKNNGKI	600
Sbjct	541	.....	600
Query	601	ELIKMFDKQQANTIFWSPQGQFVVLAGLRSMNGALAFVDTSDCTVMNIAEHYMASDVEWD	660
Sbjct	601	.....	660
Query	661	PTGRYVVTSSVSWSHKVDNAYWLWTFQGRLLQKNNKDRFCQLLWRPRPPTLLSQEQIKQI	720
Sbjct	661	.....	720
Query	721	KKDLKKYSKIFEQKDRLSQSKASKELVERRRTMMEDFRKYRKMAQELYMEQKNERLELRG	780
Sbjct	721	.....	780
Query	781	GVDTDELDSNVDDWEEETIEFFVTEEIPLGNQE 814	
Sbjct	781	..... 814	

>gb|EAW87239.1| **G** eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa,  
isoform CRA\_c [Homo sapiens]  
Length=819

Score = 1570 bits (4065), Expect = 0.0, Method: Composition-based stats.  
Identities = 812/819 (99%), Positives = 813/819 (99%), Gaps = 5/819 (0%)

Query	1	MQDAENVAVPEAAEERAEPGQQQPAAEPPPAEGLLRPAGPGAPEAAAGTEASSEEVGIAEA	60
Sbjct	1	.....	60

Query	61	GPEPEVRTEPAAEAEAASGPSESPSPAAEELPGSHAEPVPAQGEAPGEQARDERSDSR	120
Sbjct	61	...S.....	120
Query	121	AQAVSEDAGGNEGRAAEAEPRALENGDADEPSFSDPEDFVDDVSEEELLGDVLKDRPQEA	180
Sbjct	121	.....	180
Query	181	DGIDSVIVVDNVPQVGPDRLEKLKNVIHKIFSKFGKITNDFYPEEDGKTKGYIFLEYASP	240
Sbjct	181	.....	240
Query	241	AHAVDAVKNADGYKLDKQHTFRVNLFTDFDKYMTISDEWDIPEKQPFKDLGNLRYWLEEA	300
Sbjct	241	.....	300
Query	301	ECRDQYSVIFESGDRTSIFWNDVKDPVSIEERARWTETYVRWSPKGYLATFHQRGIALW	360
Sbjct	301	.....	360
Query	361	GGEKFKQIQRFHQGVQLIDFSPCERYLVTFSPPLMDTQDDPQAIIIWDILTGHKKRGFHC	420
Sbjct	361	.....	420
Query	421	ESSAHWPIFKWSDGKFFARMTLDTLSTIYETPSMGLLDKKSLKISGIKDFSWSPPGNNIIA	480
Sbjct	421	.....	480
Query	481	FWVPEDKDIPARVTLMLPTRLQEIIRVNLFNVDCKLHWQKNGDYLCVKVDRTPKGTQGV	540
Sbjct	481	.....	540
Query	541	VTNFEIFRMREKQVPVDVEMK-----ETIIAFAWEPNGSKFAVLHGEAPRISVSFYHVK	595
Sbjct	541	.....GKLYFK.....	600
Query	596	NNGKIELIKMFDKQANTIFWSPQGFVVLAGLRSMNGALAFVDTSDCTVMNIAEHYMAS	655
Sbjct	601	.....	660
Query	656	DVEWDPTGRYVVTSSVSWWSHKVDNAYWLWTFQGRLLQKNNKDRFCQLLRPRPPTLLSQE	715
Sbjct	661	.....	720
Query	716	QIKQIKKDLKKYSKIFEQKDRLSQSKASKELVERRRTMMEDFRKYRKMAQELYMEQKNER	775
Sbjct	721	.....	780
Query	776	LELRGGVDTDELDSNVDDWEEETIEFFVTEEIIPLGNQE	814
Sbjct	781	.....	819

>gb|EAL23952.1| **G** eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa  
[Homo sapiens]

gb|EAW87238.1| **G** eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa,  
isoform CRA\_b [Homo sapiens]  
Length=775

Score = 1528 bits (3955), Expect = 0.0, Method: Composition-based stats.  
Identities = 774/814 (95%), Positives = 774/814 (95%), Gaps = 39/814 (4%)

Query	1	MQDAENVAVPEAAEERAEPGQQQPAAEPPPAEGLLRPAGPGAPEAAAGTEASSEEVGIAEA	60
Sbjct	1	.....	60
Query	61	GPEPEVRTEPAAEAEAASGPSESPSPAAEELPGSHAEPVPAQGEAPGEQARDERSDSR	120
Sbjct	61	...S.....	81
Query	121	AQAVSEDAGGNEGRAAEAEPRALENGDADEPSFSDPEDFVDDVSEEELLGDVLKDRPQEA	180
Sbjct	82	.....	141
Query	181	DGIDSVIVVDNVPQVGPDRLEKLKNVIHKIFSKFGKITNDFYPEEDGKTKGYIFLEYASP	240
Sbjct	142	.....	201
Query	241	AHAVDAVKNADGYKLDKQHTFRVNLFTDFDKYMTISDEWDIPEKQPFKDLGNLRYWLEEA	300
Sbjct	202	.....	261
Query	301	ECRDQYSVIFESGDRTSIFWNDVKDPVSIEERARWTETYVRWSPKGYLATFHQRGIALW	360
Sbjct	262	.....	321
Query	361	GGEKFKQIQRFHQGVQLIDFSPCERYLVTFSPPLMDTQDDPQAIIIWDILTGHKKRGFHC	420
Sbjct	322	.....	381
Query	421	ESSAHWPIFKWSDGKFFARMTLDTLSTIYETPSMGLLDKKSLKISGIKDFSWSPPGNNIIA	480
Sbjct	382	.....	441
Query	481	FWVPEDKDIPARVTLMLPTRLQEIIRVNLFNVDCKLHWQKNGDYLCVKVDRTPKGTQGV	540
Sbjct	442	.....	501
Query	541	VTNFEIFRMREKQVPVDVEMKETIIAFAWEPNGSKFAVLHGEAPRISVSFYHVKNNNGKI	600
Sbjct	502	.....	561

Query	601	ELIKMFDKQQANTIFWSPQGQFVVLAGLRSMNGALAFVDTSDCTVMNIAEHYMASDVEWD	660
Sbjct	562	.....	621
Query	661	PTGRYVVTSSVSWSHKVDNAYWLWTFQGRLLQKNNKDRFCQLLWRPRPPTLLSSEQEIQKI	720
Sbjct	622	.....	681
Query	721	KKDLKKYSKIFEQKDRLSQSKASKELVERRRTMMEDFRKYRKMAQELYMEQKNERLELRG	780
Sbjct	682	.....	741
Query	781	GVDTDELDSNVDDWEEETIEFFVTEEIIPLGNQE	814
Sbjct	742	.....	775

>gb|AAH23767.1| **UG** Eif3s9 protein [Mus musculus]

gb|AAH51065.1| **UG** Eif3s9 protein [Mus musculus]

Length=970

Score = 1451 bits (3755), Expect = 0.0, Method: Composition-based stats.  
Identities = 732/804 (91%), Positives = 754/804 (93%), Gaps = 15/804 (1%)

Query	1	MQDAENVAVPEAAEERAEPGQQPAAEPPPAEGLLRPAGPGAPEAAAGTEASSEEVGIAEA	60
Sbjct	1	.....AR....S.S..TD---EA..S.GS.VGQ..DAE.D---...	54
Query	61	GPEPEVRTEPAA--EAEAASGPSESPPPAEELPGSHAEPVPAQGEAPGEQARDERSD	118
Sbjct	55	.....AK...QS.E.T.TS.AA..T.QS..RS.SQ---SA.GKA..V.....GHP.-	111
Query	119	SRAQAVSEDAGGNEGRAAAEAPRALENGDADEPSFSDPEDFVDDVSEELLGDVLKDRPQ	178
Sbjct	112	----.GA.EE..SD.S.....E.....	167
Query	179	EADGIDSVIVVDNVPQVGPDRLEKLKNVIHKIFSKFGKITNDFYPEEDGKTGKIIFLEYA	238
Sbjct	168	.....I..Y.....	227
Query	239	SPAHAVIDAVKNADGYKLDKQHTFRVNLFTDFDKYMTISDEWDIPEKQPFKDLGNLRYWLE	298
Sbjct	228	.....	287
Query	299	EAECRDQYSVIFESGDRTSIFWNDVKDPVSIEERARWTETYVRWSPKGTYLATFHQRGIA	358
Sbjct	288	.....	347
Query	359	LWGGEKFKQIQRFHQGVQLIDFSPCERYLVTFSPMLDTQDDPQAIIIWDILTGHKKRGF	418
Sbjct	348	....D.....	407
Query	419	HCESSAHWPIFKWSDGKFFARMTLDTLISYETPSMGLLDKKSLKISGIKDFSWSPGGNI	478
Sbjct	408	.....	467
Query	479	IAFWVPEDKDIPARVTLMLPTRQEIRVRNLFNVVDCKLHWQKNGDYLCVKVDRTPKGTQ	538
Sbjct	468	.....	527
Query	539	GVVTNFEIFRMREKQVPVDVEMKETIIAFAWEPNGSKFAVLHGEAPRISVSFYHVKNNG	598
Sbjct	528	.....S..	587
Query	599	KIELIKMFDKQQANTIFWSPQGQFVVLAGLRSMNGALAFVDTSDCTVMNIAEHYMASDVE	658
Sbjct	588	.....	647
Query	659	WDPTGRYVVTSSVSWSHKVDNAYWLWTFQGRLLQKNNKDRFCQLLWRPRPPTLLSSEQEIK	718
Sbjct	648	.....D...	707
Query	719	QIKDLKKYSKIFEQKDRLSQSKASKELVERRRTMMEDFRKYRKMAQELYMEQKNERLEL	778
Sbjct	708	.....Q.....K.....	767
Query	779	RGVDTDELDSNVDDWEEETIEFF	802
Sbjct	768	.....	791

>ref|NP\_598677.1| **UG** eukaryotic translation initiation factor 3, subunit 9 [Mus musculus]

sp|Q8JZQ9|IF39\_MOUSE **G** Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p116)

gb|AAH31704.1| **UG** Eukaryotic translation initiation factor 3, subunit 9 (eta) [Mus musculus]

dbj|BAC28445.1| **UG** unnamed protein product [Mus musculus]

dbj|BAE39671.1| **UG** unnamed protein product [Mus musculus]

dbj|BAE42128.1| **UG** unnamed protein product [Mus musculus]

gb|EDL19120.1| eukaryotic translation initiation factor 3, subunit 9 (eta) [Mus musculus]  
Length=803

Score = 1437 bits (3721), Expect = 0.0, Method: Composition-based stats.  
Identities = 742/816 (90%), Positives = 766/816 (93%), Gaps = 15/816 (1%)

Query	1	MQDAENVAVPEAAEERAEPGQQQPAAEPPPAEGLLRPAGPGAPEAAAGTEASSEEVGIAEA	60
Sbjct	1	.....AR....S.S..TD---EA..S.GS.VGQ..DAE.D---...	54
Query	61	GPEPEVRTEPAA--EAEAASGPSESPPPAEELPGSHAEPVPAQGEAPGEQARDERSD	118
Sbjct	55	.....AK...QS.E.T.TS.AA..T.QS..RS.SQ---SA.GKA..V.....GHP.-	111
Query	119	SRAQAVSEDAGGNEGRAAAEAPRALENGDADEPSFSDPEDFVDDVSEEEELLDVLRKDRPQ	178
Sbjct	112	----.GA.EE..SD.S.....E.....	167
Query	179	EADGIDSVIVVDNVPQVGPDRLEKLKNVIHKIFSKFGKITNDFYPEEDGKTKGYIFLEYA	238
Sbjct	168	.....I..Y.....	227
Query	239	SPAHAVIDAVKNADGYKLDKQHTFRVNLFTDFDKYMTISDEWDIPEKQPFKDLGNLRYWLE	298
Sbjct	228	.....	287
Query	299	EAECRDQYSVIFESGDRTSIFWNDVKDPVSIERARWTETYVRWSPKGYLATFHHQORGIA	358
Sbjct	288	.....	347
Query	359	LWGGEKFKQIQRFHQVQLIDFSPCERYLVTFSPMLDTQDDPQAIIIWDILTGHKKRGF	418
Sbjct	348	....D.....	407
Query	419	HCESSAHWPIFKWSDGKFFARMTLDTLISYETPSMGLLDKKSLKISGIKDFSWSPPGNI	478
Sbjct	408	.....	467
Query	479	IAFWVPEDKDIPARVTLMQLPTRQEIRVRNLFNVVDCKLHWQKNGDYLCVKVDRTPKGTQ	538
Sbjct	468	.....	527
Query	539	GVVTNFEIFRMREKQVPVDVEMKETIIAFAWEPNGSKFAVLHGEAPRISVSFYHVKNNG	598
Sbjct	528	.....S..	587
Query	599	KIELIKMFDKQANTIFWSPQGQFVVLAGLRSMNGALAFVDTSDCTVMNIAEHYMASDVE	658
Sbjct	588	.....	647
Query	659	WDPTGRYVVTSSVSWSHKVDNAYWLWTFQGRLLQKNNKDRFCQLLWRPRPPTLLSQEQIK	718
Sbjct	648	.....D...	707
Query	719	QIKKDLKKYSKIFEQKDRLSQSKASKELVERRRTMMEDFRKYRKMAQELYMEQKNERLEL	778
Sbjct	708	.....Q.....K.....	767
Query	779	RGGVDTDDELDSNVDDWEEETIEFFVTEEIIPLGNOE	814
Sbjct	768	.....V....S..	803

>ref|NP\_001026810.1| **UG** eukaryotic translation initiation factor 3, subunit 9 (eta) [Rattus norvegicus]

sp|Q4G061|IF39\_RAT **G** Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta)

gb|AAH98728.1| **UG** Eukaryotic translation initiation factor 3, subunit 9 (eta) [Rattus norvegicus]

gb|EDL89734.1| eukaryotic translation initiation factor 3, subunit 9 (eta) [Rattus norvegicus]  
Length=797

Score = 1425 bits (3688), Expect = 0.0, Method: Composition-based stats.  
Identities = 735/814 (90%), Positives = 759/814 (93%), Gaps = 17/814 (2%)

Query	1	MQDAENVAVPEAAEERAEPGQQQPAAEPPPAEGLLRPAGPGAPEAAAGTEASSEEVGIAEA	60
Sbjct	1	.....A.....AR...VS.S..TD---EA..S.GS.VGR..DAE.D---...	54
Query	61	GPEPEVRTEPAAEAEAASGPSESPPPAEELPGSHAEPVPAQGEAPGEQARDERSDSR	120
Sbjct	55	R.....AK...QS.-----E.TAAS...SPT.Q.AQ..SA.GKA..G.....-----H	103
Query	121	AQAVSEDAGGNEGRAAAEAPRALENGDADEPSFSDPEDFVDDVSEEEELLDVLRKDRPQEA	180
Sbjct	104	PS.RA.EE..SD.S.....E.....	163
Query	181	DGIDSVIVVDNVPQVGPDRLEKLKNVIHKIFSKFGKITNDFYPEEDGKTKGYIFLEYASP	240
Sbjct	164	.....I..Y.....	223
Query	241	AHAVIDAVKNADGYKLDKQHTFRVNLFTDFDKYMTISDEWDIPEKQPFKDLGNLRYWLEEA	300
Sbjct	224	.....	283
Query	301	ECRDQYSVIFESGDRTSIFWNDVKDPVSIERARWTETYVRWSPKGYLATFHHQORGIALW	360
Sbjct	284	.....	343
Query	361	GGEKFKQIQRFHQVQLIDFSPCERYLVTFSPMLDTQDDPQAIIIWDILTGHKKRGFHC	420
Sbjct	344	..D.....	403

Query	421	ESSAHWPIFKWSDGKFFARMTLDTLSIYETPSMGLLDKSLKISGIKDFSWSPPGNIIA	480
Sbjct	404	.....	463
Query	481	FWVPEDKDI PARVTLMQLPTRQEIRVRNLFNVVDCKLHWQKNGDYLCVKVDRTPKGTOGV	540
Sbjct	464	.....	523
Query	541	VTNFEIFRMREKQVPVDVEMKETIIAFAWEPNGSKFAVLHGEAPRISVSFYHVKNNGKI	600
Sbjct	524	.....S....	583
Query	601	ELIKMFDKQQANTIFWSPQGQFVVLAGLRSMNGALAFVDTSDCTVMNIAEHYMASDVEWD	660
Sbjct	584	.....	643
Query	661	PTGRYVVTSSVSWWSHKVDNAYWLWTFQGRLLQKNNKDRFCQLLWRPRPPTLLSQEQIKQI	720
Sbjct	644	.....D.....	703
Query	721	KKDLKKYSKIFEQKDRLSQSKASKELVERRRTMMEDFRKYRKMAQELYMEQKNERLELRG	780
Sbjct	704	.....Q.....K.....	763
Query	781	GVDTDELDSNVDDWEEETIEFFVTEEIPLGNQE	814
Sbjct	764	.....V....S..	797

>ref|XP\_001256599.1| **UG** PREDICTED: similar to eukaryotic translation initiation factor  
[Bos taurus]  
Length=1086

Score = 1398 bits (3618), Expect = 0.0, Method: Composition-based stats.  
Identities = 718/818 (87%), Positives = 736/818 (89%), Gaps = 32/818 (3%)

Query	1	MQDAENVAVPEAAEERAEPGQQQPAAEPPPAEGLLRPAGPGAPEAAGTEASSEEVGIAEA	60
Sbjct	297	.....A.....Q.....PE.A....S.GAEVA.----.VQ....G.D-----V..	346
Query	61	GPEPE---VRTEPAAEAAASGPSESPSPAAEELPGSHAEPVPAQGEAPGEQARDER	116
Sbjct	347	..G..GPAE..LS.RPTG.---.KADATPGATPPPEE.S.Q---LA....A...Q.AA	399
Query	117	SDSRAQAVSEDAAGNEGRAAEAPRALENGDADEPSFSDPEDFVDDVSEELGLDVLKDR	176
Sbjct	400	AEAGSEGAGG.PD.-----A.D.G.....A.....	448
Query	177	PQEADGIDSVIVVDNVPQVGPDRLEKLKNVIHKIFSKFGKITNDFYPEEDGKTKGYIFLE	236
Sbjct	449	.....R.....	508
Query	237	YASPAHAVDAVKNADGYKLDKQHTFRVNLFTDFDKYMTISDEWDIPEKQPFKDLGNLRYW	296
Sbjct	509	.....L.....	568
Query	297	LEEAECDQYSVIFESGDRTSIFWNDVKDPVSIEERARWTETTYVRWSPKGTYLATFHQRG	356
Sbjct	569	.....	628
Query	357	IALWGGEKFKQIQRFHQGVQLIDFSPCERYLVTFSPPLMDTQDDPQAIIIWDILTGHKKR	416
Sbjct	629	.....Q...	688
Query	417	GFHCESSAHWPIFKWSDGKFFARMTLDTLSIYETPSMGLLDKSLKISGIKDFSWSPPG	476
Sbjct	689	.....	748
Query	477	NIIAFWVPEDKDI PARVTLMQLPTRQEIRVRNLFNVVDCKLHWQKNGDYLCVKVDRTPKG	536
Sbjct	749	.....	808
Query	537	TQGVVTNFEIFRMREKQVPVDVEMKETIIAFAWEPNGSKFAVLHGEAPRISVSFYHVKN	596
Sbjct	809	.....	868
Query	597	NGKIELIKMFDKQQANTIFWSPQGQFVVLAGLRSMNGALAFVDTSDCTVMNIAEHYMASD	656
Sbjct	869	.....	928
Query	657	VEWDPTGRYVVTSSVSWWSHKVDNAYWLWTFQGRLLQKNNKDRFCQLLWRPRPPTLLSQEQ	716
Sbjct	929	.....S.....D.	988
Query	717	IKQIKKDLKKYSKIFEQKDRLSQSKASKELVERRRTMMEDFRKYRKMAQELYMEQKNERL	776
Sbjct	989	.....A..	1048
Query	777	ELRGGVDTDELDSNVDDWEEETIEFFVTEEIPLGNQE	814
Sbjct	1049	.....	1086

>ref|XP\_001379111.1| **G** PREDICTED: similar to eukaryotic translation initiation factor  
[Monodelphis domestica]  
Length=815

Score = 1354 bits (3504), Expect = 0.0, Method: Composition-based stats.  
Identities = 709/839 (84%), Positives = 734/839 (87%), Gaps = 49/839 (5%)

Query	1	MQDAENVAVPEAAEERAEPGQQQPAAEPPPAEGLLRPAGPGA-----PEAAGT	48
Sbjct	1	.....Q....E...AAEE.-----PE.....QEAAAAAAVLV..VK.-	53
Query	49	EASSEEVGIAEAGPEPEVRTEPAAEAEAASGPSESPPPA-----AEELPGSH	96
Sbjct	54	.KGD TT.SVVKP.S...AIVKLL..EK.VVE.ASAEP..LVSPPPGESQPPPTDKV.EPK	113
Query	97	AEPVPVPAQGEAPGEQARDERSDSRAQAVSEDAGGNEGRAAAEAPRALENG-DADEPSFSD	155
Sbjct	114	....AAKEEKREEKEKE..NK-----E....Q.R...SNEE..I....	156
Query	156	PEDFVDDVSEEEELLGDVLDKDRPQADGIDSVIVVDNVPQVGPDRLEKLKNVIHKIFSKFG	215
Sbjct	157	..G....I..D.....	216
Query	216	KITNDFYPEEDGKTKGYIFLEYASPAHAVDAVKNADGYKLDKQHTFRVNLFTDFDKYMTI	275
Sbjct	217	.....Y.....V.....L.....	276
Query	276	SDEWDIPEKQPFKDLGNLRYWLEEAECRDQYSVIFESGDRTSIFWNDVKDPVSIEERARW	335
Sbjct	277	.....	336
Query	336	TETYVRWSPKGTYLATFHQRGIALWGGEKFKQIQRFHQGVQLIDFSPCERYLVTFSPLM	395
Sbjct	337	.....	396
Query	396	DTQDDPQAI I IWDILTGHKKRGFHCESAHWPIFKWSHDGKFFARMTLDTLSIYETPSMG	455
Sbjct	397	.....Q.....M.....	456
Query	456	LLDKKSLKISGIKDFSWSPGGNIIAFWVPEDKDIPARVTLMQLPTRQEI RVRNLFNVVDC	515
Sbjct	457	.....P.....S.....	516
Query	516	KLHWQKNGDYLCVKVDRTPKG TQGVVTNFEI FRMREKQVPVDVEMKETIIAFAWEPNGS	575
Sbjct	517	.....S.....	576
Query	576	KFAVLHGEAPRISVSFYHVKNNGKIELIKMFDKQQANTIFWSPQGFVVLAGLRSMNGAL	635
Sbjct	577	.....	636
Query	636	AFVDTSDCTVMNIAEHYMASDVEWDPTGRYVVTSVSWWSHKVDNAYWLWTFQGRLLQKNN	695
Sbjct	637	.....M.....	696
Query	696	KDRFCQLLWRPRPPTLLSQEQIKQIKKDLKKYSKIFEQKDRLSQSKASKELVERRRTMME	755
Sbjct	697	.....D.....R.....	756
Query	756	DFRKYRKMAQELYMEQKNERLELRGGVDTDELDSNVDDWEEETIEFFVTEEI I PLGNQE	814
Sbjct	757	.....	815

>ref|XP\_850719.1| **UG** PREDICTED: similar to Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p116) (eIF3 p110) (eIF3b) isoform 2 [Canis familiaris]  
Length=751

Score = 1349 bits (3492), Expect = 0.0, Method: Composition-based stats.  
Identities = 713/814 (87%), Positives = 726/814 (89%), Gaps = 63/814 (7%)

Query	1	MQDAENVAVPEAAEERAEPGQQQPAAEPPPAEGLLRPAGPGAPEAAAGTEASSEEVGIAEA	60
Sbjct	1	.....A.....Q.T..V.....G.EPP..P....Q...SG.DD-----	53
Query	61	GPEPEVRTEPAAEAEAASGPSESPPPAEELPGSHAEPVPVPAQGEAPGEQARDERSDSR	120
Sbjct	54	....D-----A...G.AAAEA.	74
Query	121	AQAVSEDAGGNEGRAAAEAPRALENGDADEPSFSDPEDFVDDVSEEEELLGDVLDKDRPQEA	180
Sbjct	75	SEGAGG-----D.G.....I.....	117
Query	181	DGIDSVIVVDNVPQVGPDRLEKLKNVIHKIFSKFGKITNDFYPEEDGKTKGYIFLEYASP	240
Sbjct	118	.....T.....	177
Query	241	AHAVDAVKNADGYKLDKQHTFRVNLFTDFDKYMTISDEWDIPEKQPFKDLGNLRYWLEEA	300
Sbjct	178	...L.....	237
Query	301	ECRDQYSVIFESGDRTSIFWNDVKDPVSIEERARWTETYVRWSPKGTYLATFHQRGIALW	360
Sbjct	238	.....	297
Query	361	GGEKFKQIQRFHQGVQLIDFSPCERYLVTFSPLM DTQDDPQAI I IWDILTGHKKRGFHC	420
Sbjct	298	.....G.....Q.....	357
Query	421	ESSAHWPIFKWSHDGKFFARMTLDTLSIYETPSMGLLDKKSLKISGIKDFSWSPGGNIIA	480
Sbjct	358	.....	417
Query	481	FWVPEDKDIPARVTLMQLPTRQEI RVRNLFNVVDC KLHWQKNGDYLCVKVDRTPKG TQGV	540
Sbjct	418	.....	477
Query	541	VTNFEI FRMREKQVPVDVEMKETIIAFAWEPNGSKFAVLHGEAPRISVSFYHVKNNGKI	600

Sbjct	478	.....	537
Query	601	ELIKMFDKQQANTIFWSPQGQFVVLAGLRSMNGALAFVDTSDCTVMNIAEHYMASDVEWD	660
Sbjct	538	.....	597
Query	661	PTGRYVVTSSVSWWSHKVDNAYWLWTFQGRLLQKNNKDRFCQLLWRPRPPTLLSSEQEIKQI	720
Sbjct	598	.....D.....	657
Query	721	KKDLKKYSKIFEQKDRLSQSKASKELVERRRTMMEDFRKYRKMAQELYMEQKNERLELRG	780
Sbjct	658	.....S.....	717
Query	781	GVDTDELDSNVDDWEEETIEFFVTEEIIPLGNQE	814
Sbjct	718	.....E.....	751

>ref|XP\_536894.2| **UG** PREDICTED: similar to Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p116) (eIF3 p110) (eIF3b) isoform 1 [Canis familiaris]

ref|XP\_862080.1| **UG** PREDICTED: similar to Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p116) (eIF3 p110) (eIF3b) isoform 3 [Canis familiaris]

ref|XP\_862108.1| **UG** PREDICTED: similar to Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p116) (eIF3 p110) (eIF3b) isoform 4 [Canis familiaris]  
Length=785

Score = 1335 bits (3455), Expect = 0.0, Method: Composition-based stats.  
Identities = 656/664 (98%), Positives = 661/664 (99%), Gaps = 0/664 (0%)

Query	151	PSFSDPEDFVDDVSEELLGDVLKDRPQEADGIDSVIVVDNVPQVGPDRLEKLKNVIHKE	210
Sbjct	122	.....I.....	181
Query	211	FSKFGKITNDFYPEEDGKTGKYIFLEYASPAHAVDAVKNDGYKLDKQHTFRVNLFTDFD	270
Sbjct	182	.....T.....L.....	241
Query	271	KYMTISDEWDIPEKQPFKDLGNLRYWLEEAECRDQYSVIFESGDRTSIFWNDVKDPVSIE	330
Sbjct	242	.....	301
Query	331	ERARWTETYVRWSPKGTYLATFHQRGIALWGGEKFKQIQRFHQGVQLIDFSPCERYLVT	390
Sbjct	302	.....	361
Query	391	FSPLMDTQDDPQAIIIWDILTGHKKRGFHCESAHWPFIKWSHDGKFFARMTLDTLSIYE	450
Sbjct	362	.....G.....Q.....	421
Query	451	TPSMGLLDKSKSLKISGIKDFSWSPGGNIIAFWVPEDKDIPARVTLMLPTRQEIRVRNLF	510
Sbjct	422	.....	481
Query	511	NVVDCKLHWQKNGDYLCVKVDRTPKGTQGVVTNFEIFRMREKQVPVDVEMKETIIAFAW	570
Sbjct	482	.....	541
Query	571	EPNGSKFAVLHGEAPRISVSFYHVKNNGKIELIKMFDKQQANTIFWSPQGQFVVLAGLRS	630
Sbjct	542	.....	601
Query	631	MNGALAFVDTSDCTVMNIAEHYMASDVEWDPTGRYVVTSSVSWWSHKVDNAYWLWTFQGR	690
Sbjct	602	.....	661
Query	691	LQKNNKDRFCQLLWRPRPPTLLSSEQEIKQIKDLKKYSKIFEQKDRLSQSKASKELVERR	750
Sbjct	662	.....D.....	721
Query	751	RTMMEDFRKYRKMAQELYMEQKNERLELRGGVDTDELDSNVDDWEEETIEFFVTEEIIPL	810
Sbjct	722	.....S.....E.....	781
Query	811	GNQE	814
Sbjct	782	....	785

>ref|XP\_001513573.1| **G** PREDICTED: similar to eukaryotic translation initiation factor [Ornithorhynchus anatinus]  
Length=692

Score = 1316 bits (3407), Expect = 0.0, Method: Composition-based stats.  
Identities = 634/651 (97%), Positives = 646/651 (99%), Gaps = 0/651 (0%)

Query	164	SEELLGDVLKDRPQEADGIDSVIVVDNVPQVGPDRLEKLKNVIHKEFSKFGKITNDFYP	223
Sbjct	42	NKKK.....M.....Y..	101
Query	224	EEDGKTKGYIFLEYASPAHAVDAVKNDGYKLDKQHTFRVNLFTDFDKYMTISDEWDIPE	283
Sbjct	102	.....V.....L.....	161

Query	284	KQPFKDLGNLRYWLEEAACRDQYSVIFESGDRTSIFWNDVKDPVSIEERARWTETTYVRWS	343
Sbjct	162	.....	221
Query	344	PKGTYLATFHQRGIALWGGEKFKQIQRFHQGVQLIDFSPCERYLVTFSPPLMDTQDDPQA	403
Sbjct	222	.....	281
Query	404	IIIWDILTGHKKRGFHCESAHWPIFKWSDGKFFARMTLDTLSIYETPSMGLLDKKSLLK	463
Sbjct	282	.....Q.....V.....	341
Query	464	ISGIKDFSWSPGGNIIAFWVPEDKDIPARVTLMQLPTRQEIRVRNLFNVVDCKLHWQKNG	523
Sbjct	342	.....	401
Query	524	DYLCVKVDRTPKGTQGVVTNFEIFRMREKQVPVDVEMKETIIAFAWEPNGSKFAVLHGE	583
Sbjct	402	.....S.....	461
Query	584	APRISVSFYHVKNNGKIELIKMFDKQQANTIFWSPQGGFVVLAGLRSMNGALAFVDTSDC	643
Sbjct	462	T.....	521
Query	644	TVMNIAEHYMASDVEWDPTGRYVVTSSVSWWSHKVDNAYWLWTFQGRLLQKNNKDRFCQLL	703
Sbjct	522	.M.....	581
Query	704	WRPRPPTLLSQEQIKQIKKDLKKYSKIFEQKDRLSQSKASKELVERRRTMMEDFRKYRKM	763
Sbjct	582	.....T.....D.....R.....	641
Query	764	AQELYMEQKNERLELRGGVDTDELDSNVDDWEEETIEFFVTEEIIPLGNQE	814
Sbjct	642	.....L.....	692

>gb|AAH07175.1| **UG** Eif3s9 protein [Mus musculus]  
Length=641

Score = 1307 bits (3383), Expect = 0.0, Method: Composition-based stats.  
Identities = 632/641 (98%), Positives = 640/641 (99%), Gaps = 0/641 (0%)

Query	174	KDRPQEADGIDSVIVVDNVPQVGPDRLEKLKNVIHKIFSKFGKITNDFYPEEDGKTKGYI	233
Sbjct	1	.....I..Y.....	60
Query	234	FLEYASPAHAVDAVKNAAGYKLDKQHTFRVNLFTDFDKYMTISDEWDIPEKQPFKDLGNL	293
Sbjct	61	.....	120
Query	294	RYWLEEAACRDQYSVIFESGDRTSIFWNDVKDPVSIEERARWTETTYVRWSPKGTYLATFH	353
Sbjct	121	.....	180
Query	354	QRGIALWGGEKFKQIQRFHQGVQLIDFSPCERYLVTFSPPLMDTQDDPQAIIWDILTGH	413
Sbjct	181	.....D.....	240
Query	414	KKRGFHCESAHWPIFKWSDGKFFARMTLDTLSIYETPSMGLLDKKSLLKISGIKDFSW	473
Sbjct	241	.....	300
Query	474	PGGNIIAFWVPEDKDIPARVTLMQLPTRQEIRVRNLFNVVDCKLHWQKNGDYLCVKVDRT	533
Sbjct	301	.....	360
Query	534	PKGTQGVVTNFEIFRMREKQVPVDVEMKETIIAFAWEPNGSKFAVLHGEAPRISVSFYH	593
Sbjct	361	.....	420
Query	594	VKNNGKIELIKMFDKQQANTIFWSPQGGFVVLAGLRSMNGALAFVDTSDCTVMNIAEHY	653
Sbjct	421	..S.....	480
Query	654	ASDVEWDPTGRYVVTSSVSWWSHKVDNAYWLWTFQGRLLQKNNKDRFCQLLWRPRPPTLLS	713
Sbjct	481	.....	540
Query	714	QEIQIKQIKKDLKKYSKIFEQKDRLSQSKASKELVERRRTMMEDFRKYRKMAQELYMEQKN	773
Sbjct	541	.D.....Q.....K...	600
Query	774	ERLELRGGVDTDELDSNVDDWEEETIEFFVTEEIIPLGNQE	814
Sbjct	601	.....V....S..	641

>gb|AAH09986.1|AAH09986 **UG** Unknown (protein for IMAGE:4124553) [Homo sapiens]  
Length=622

Score = 1276 bits (3303), Expect = 0.0, Method: Composition-based stats.  
Identities = 621/623 (99%), Positives = 621/623 (99%), Gaps = 1/623 (0%)

Query	192	VPQVGPDRLEKLKNVIHKIFSKFGKITNDFYPEEDGKTKGYIFLEYASPAHAVDAVKNA	251
Sbjct	1	.....	60
Query	252	GYKLDKQHTFRVNLFTDFDKYMTISDEWDIPEKQPFKDLGNLRYWLEEAACRDQYSVIFE	311



Sbjct	61	.....	120
Query	312	SGDRTSIFWNDVKDPVSIEERARWTETVVRWSPKGTYLATFHQRGIALWGGEKFKQIQRF	371
Sbjct	121	.....	180
Query	372	SHQGVQLIDFSPCERYLVTFSPMLDTQDDPQAIIIWDILTGHKKRGFHCESAHWPFIKW	431
Sbjct	181	.....	240
Query	432	SHDGKFFARMTLDTLSIYETPSMGLLDKKSLKISGIKDFSWSPGGNIIAFWVPEDKDIPA	491
Sbjct	241	.....	300
Query	492	RVTLMQLPTRQEIRVRNLFNVVDCKLHWQKNGDYLCVKVDRTPKGTOGVVTNFEIFRMRE	551
Sbjct	301	.....Y.....	359
Query	552	KQVPVDVDEMKETIIAFWEPNGSKFAVLHGEAPRISVSFYHVKNNGKIELIKMFDKQQA	611
Sbjct	360	.....	419
Query	612	NTIFWSPQGQFVVLAGLRSMNGALAFVDTSDCTVMNIAEHYMASDVEWDPTGRYVVTSVS	671
Sbjct	420	.....	479
Query	672	WWSHKVDNAYWLWTFQGRLLQKNNKDRFCQLLWRPRPPTLLSQEQIKQIKKDLKKYSKIF	731
Sbjct	480	.....	539
Query	732	EQKDRLSQSKASKELVERRRTMMEDFRKYRKMAQELYMEQKNERLELRGGVDTDELDSNV	791
Sbjct	540	.....	599
Query	792	DDWEEETIEFFVTEEIIPLGNQE	814
Sbjct	600	.....	622

>ref|NP\_001090004.1| **UG** hypothetical protein LOC735075 [Xenopus laevis]  
gb|AAH92246.1| **UG** MGC99017 protein [Xenopus laevis]  
Length=688

Score = 1246 bits (3223), Expect = 0.0, Method: Composition-based stats.  
Identities = 595/658 (90%), Positives = 633/658 (96%), Gaps = 0/658 (0%)

Query	153	FSDPEDFVDDVSEEEELLGDVLKDRPQEADGIDSVIVVDNVPQVGPDRLEKLKNVIHKIFS	212
Sbjct	29	.....G.E..I.D.....I.....V....	88
Query	213	KFGKITNDFYPEEDGKTGKIYIFLEYASPAHAVDAVKADGYKLDKQHTFRVNLFTDFDKY	272
Sbjct	89	....L..E...QAE.S.....L..Q.Q.....	148
Query	273	MTISDEWDIPEKQPFKDLGNLRYWLEEAECRDQYSVIFESGDRTSIFWNDVKDPVSIEER	332
Sbjct	149	.V.G...V.....F....S...DPD....F...Y.....T...E..PV...	208
Query	333	ARWTETVVRWSPKGTYLATFHQRGIALWGGEKFKQIQRFSSHQGVQLIDFSPCERYLVTF	392
Sbjct	209	.....	268
Query	393	PLMDTQDDPQAIIIWDILTGHKKRGFHCESAHWPFIKWSHDGKFFARMTLDTLSIYETP	452
Sbjct	269	.....KEE.....N.....	328
Query	453	SMGLLDKKSLKISGIKDFSWSPGGNIIAFWVPEDKDIPARVTLMQLPTRQEIRVRNLFNV	512
Sbjct	329	.....T.....M.....	388
Query	513	VDCKLHWQKNGDYLCVKVDRTPKGTOGVVTNFEIFRMREKQVPVDVDEMKETIIAFWEP	572
Sbjct	389	.....M.....DG.....	448
Query	573	NGSKFAVLHGEAPRISVSFYHVKNNGKIELIKMFDKQANTIFWSPQGQFVVLAGLRSMN	632
Sbjct	449	.....V.....Y.....L.....	508
Query	633	GALAFVDTSDCTVMNIAEHYMASDVEWDPTGRYVVTSVSWWSHKVDNAYWLWTFQGRLLQ	692
Sbjct	509	.....I.....T.....I.....M.....	568
Query	693	KNNKDRFCQLLWRPRPPTLLSQEQIKQIKKDLKKYSKIFEQKDRLSQSKASKELVERRRT	752
Sbjct	569	.....S....D.....T.....I....A	628
Query	753	MMEDFRKYRKMAQELYMEQKNERLELRGGVDTDELDSNVDDWEEETIEFFVTEEIIPL	810
Sbjct	629	...EYKT..E..TK.....TA...I.....L.....E.....V	686

>ref|NP\_001016724.1| **UG** eukaryotic translation initiation factor 3, subunit 9 eta, 116kDa [Xenopus tropicalis]  
Length=676

Score = 1223 bits (3164), Expect = 0.0, Method: Composition-based stats.  
Identities = 597/659 (90%), Positives = 632/659 (95%), Gaps = 0/659 (0%)

Query	152	SFSDPEDFVDDVSEEEELLGDVLKDRPQEADGIDSVIVVDNVPQVGPDRLEKLKNVIHKIF	211
Sbjct	16	.....G.E..I.....I.....V.....N...	75
Query	212	SKFGKITNDFYPEEDGKTKGYIFLEYASPAHAVDAVKNAADGYKLDKQHTFRVNLFTDFDK	271
Sbjct	76	.....EY...AE.T.R.....L.TQ.Q.....C.....	135
Query	272	YMTISDEWDIPEKQPFKDLGNLRYWLEEAECRDQYSVIFESGDRTSIFWNDVKDPVSIEE	331
Sbjct	136	..V.G...EA.....F....S...DPD....F...Y.....T...E..PV..	195
Query	332	RARWTETYVRWSPKGTYLATFHQRGIALWGGEKFKQIQRFHQGVQLIDFSPCERYLVTF	391
Sbjct	196	.....	255
Query	392	SPLMDTQDDPQAIIIWDILTGHKKRGFHCESSAHWPIFKWSHDGKFFARMTLDTLSIYET	451
Sbjct	256	.....KEE.....QN.....	315
Query	452	PSMGLLDKSKSLKISGIKDFSWSPGGNIIAFWVPEDKDIPARVTLMQLPTRQEIRVRNLFN	511
Sbjct	316	.....T.....S.....	375
Query	512	VVDCKLHWQKNGDYLCKVKVDRTPKGTQGVVTNFEIFRMREKQVPVDVDEMKETIIAFAWE	571
Sbjct	376	.....DG.....	435
Query	572	PNGSKFAVLHGEAPRISVSFYHVKNNGKIELIKMFDKQANTIFWSPQGGQFVVLAGLRSM	631
Sbjct	436	.....V.....Y.....L.....	495
Query	632	NGALAFVDTSDCTVMNIAEHYMASDVEWDPTGRYVVTSSVSWWSHKVDNAYWLWTFQGRL	691
Sbjct	496	.....I.....T.....M.....	555
Query	692	QKNNKDRFCQLLWRPRPPTLLSQEQIKQIKKDLKKYSKIFEQKDRLSQSKASKELVERRR	751
Sbjct	556	.....S....D.....I....	615
Query	752	TMMEDFRKYRKMAQELYMEQKNERLELRGGVDTDELDSNVDDWEEETIEFFVTEEIIPL	810
Sbjct	616	A...EYKT..E..AK.....AA...I.....V	674

>ref|XP\_862133.1| **UG** PREDICTED: similar to Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p116) (eIF3 p110) (eIF3b) isoform 5 [Canis familiaris]  
Length=741

Score = 1221 bits (3159), Expect = 0.0, Method: Composition-based stats.  
Identities = 614/664 (92%), Positives = 619/664 (93%), Gaps = 44/664 (6%)

Query	151	PSFSDPEDFVDDVSEEEELLGDVLKDRPQEADGIDSVIVVDNVPQVGPDRLEKLKNVIHKI	210
Sbjct	122	.....I.....	181
Query	211	FSKFGKITNDFYPEEDGKTKGYIFLEYASPAHAVDAVKNAADGYKLDKQHTFRVNLFTDFD	270
Sbjct	182	.....T.....L.....	241
Query	271	KYMTISDEWDIPEKQPFKDLGNLRYWLEEAECRDQYSVIFESGDRTSIFWNDVKDPVSIE	330
Sbjct	242	.....	301
Query	331	ERARWTETYVRWSPKGTYLATFHQRGIALWGGEKFKQIQRFHQGVQLIDFSPCERYLV	390
Sbjct	302	.....	357
Query	391	FSPLMDTQDDPQAIIIWDILTGHKKRGFHCESSAHWPIFKWSHDGKFFARMTLDTLSIYE	450
Sbjct	358	.....	377
Query	451	TSPMGLLDKSKSLKISGIKDFSWSPGGNIIAFWVPEDKDIPARVTLMQLPTRQEIRVRNL	510
Sbjct	378	.....	437
Query	511	NVVDCKLHWQKNGDYLCKVKVDRTPKGTQGVVTNFEIFRMREKQVPVDVDEMKETIIAFAW	570
Sbjct	438	.....	497
Query	571	EPNGSKFAVLHGEAPRISVSFYHVKNNGKIELIKMFDKQANTIFWSPQGGQFVVLAGLRS	630
Sbjct	498	.....	557
Query	631	MNGALAFVDTSDCTVMNIAEHYMASDVEWDPTGRYVVTSSVSWWSHKVDNAYWLWTFQGRL	690
Sbjct	558	.....	617
Query	691	LQKNNKDRFCQLLWRPRPPTLLSQEQIKQIKKDLKKYSKIFEQKDRLSQSKASKELVERR	750
Sbjct	618	.....D.....	677
Query	751	RTMMEDFRKYRKMAQELYMEQKNERLELRGGVDTDELDSNVDDWEEETIEFFVTEEIIPL	810
Sbjct	678	.....S.....E.....	737
Query	811	GNQE	814
Sbjct	738	.....	741